Sa247851_0026.Dna
Gcg_Geneseq_D:T19113

XP2128499

ID T19113 standard; cDNA to mRNA; 351 BP.
AC T19113;
DT 04-JUL-1996 (first entry)

DE Human gene signature HUMGS00127.
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
OS Homo sapiens.
PN WO 9514772-A1.
PD 01-JUN-1995.
PF 11-NOV-1994; 94WO-JP01916.
PR 12-NOV-1993; 93JP-0355504.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
PI Matsubara K, Okubo K;
DR WPI; 1995-206931/27.
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human

PT tissues
PS Claim 1; Page 304; 2245pp; Japanese.
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in T19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
SQ Sequence 351 BP; 123 A; 45 C; 58 G; 121 T; 4 other;

SCORES Init1: 1638 Initn: 1638 Opt: 1706 z-score: 597.6 E(): 5.9e-24
  98.9% identity in 349 bp overlap

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                                              |||||||||||| |||||| ||||||||||||
T19113                                        GATCACATTATNATAAATAAATGAAAAAAT
                                                        10         20         30

          1540       1550       1560       1570       1580       1590
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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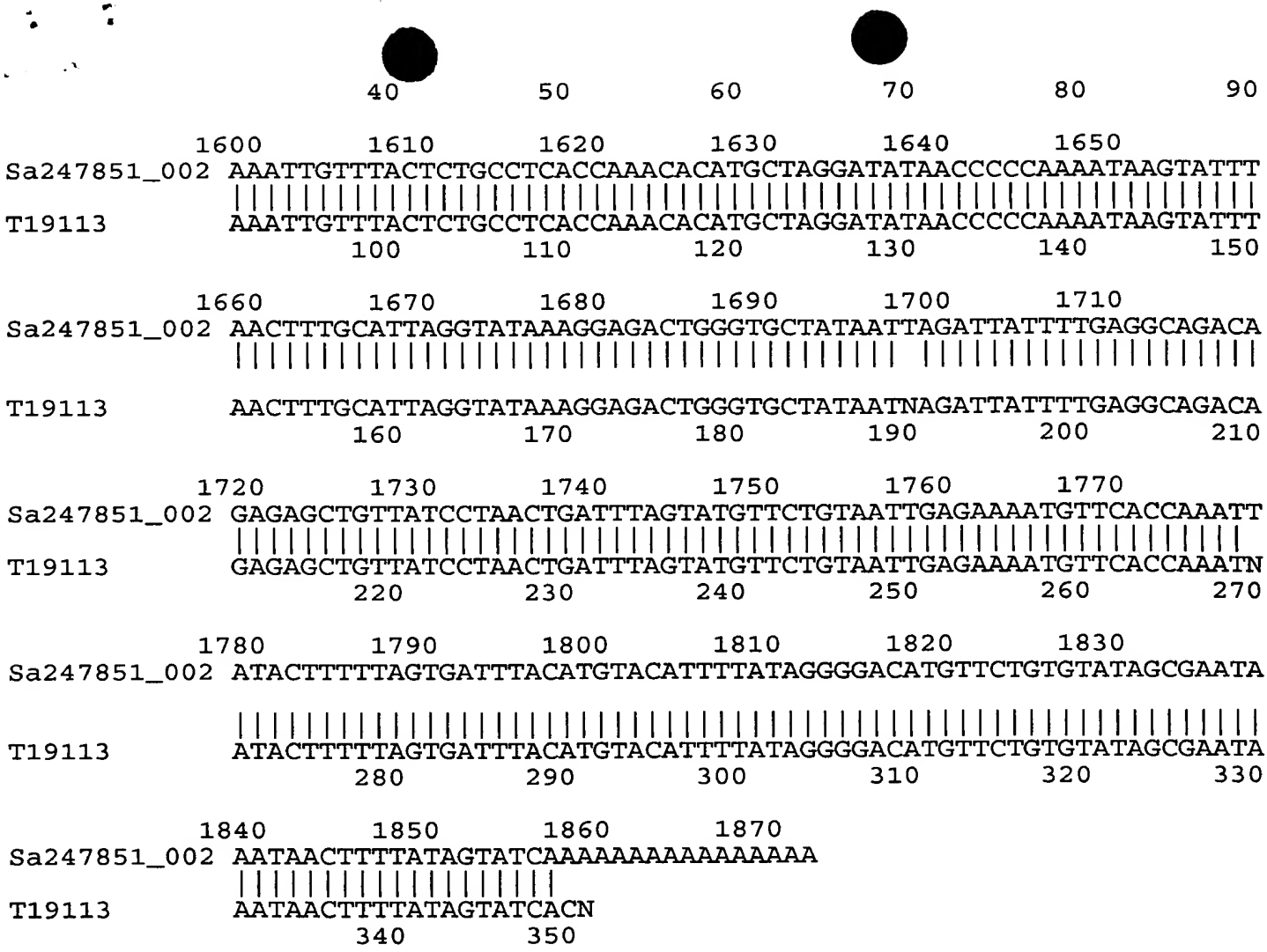
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1660 1670 1680 1690 1700 1710
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1720 1730 1740 1750 1760 1770
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1840 1850 1860 1870
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T19113 AATAACTTTTATAGTATCACN
340 350

(19) Europäisches Patentamt
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(11) Publication number: **0 679 716 A1**

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(43) Date of publication of application: **02.11.95 Bulletin 95/44**

(84) Designated Contracting States: **AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE**

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Holbeinstrasse 5
D-81679 München (DE)

(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomoly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AQ	AS	AU	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
1	GS	Sequence No.	F	MepG2	mmHL60	pmHL60+DMSO	mpHL60+TPA	40w liver	19w liver	adult liver	lung	subcutaneous adipose	aortic endothel	osteoblast	colon mucosa	small cell carcinoma of lung	retina	cerebral cortex	adenocarcinoma of lung	squamous cell carcinoma of lung	keratinocyte	fibroblast	Alzheimer disease	cerebellum	visceral fat	corneal epithelium	peripheral granulocyte	neuroblastoma	taste bud of tongue	Accession number of target mRNA	match %	match size	match starts at (GS)	match starts at (GenBank)	GenBank target size
2	00001	00001	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	H77349	95.2	461	1	2003	2691
3	00002	00002	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J05249	94.8	620	1	894	1512
4	00003	00003	3	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	X72875	91	613	1	1737	2345
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6	00005	00005	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7	00006	00006	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
8	00007	00007	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0						
9	00008	00008	3	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0						
10	00009	00009	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
11	00010	00010	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
12	00011	00011	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	Y00856	90.3	607	1	784	1397
13	00012	00012	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
14	00013	00013	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
15	00014	00014	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
16	00015	00015	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
17	00016	00016	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
18	00017	00017	25	3	2	1	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	H84711	93.1	536	1	346	874
19	00018	00018	128	17	8	2	26	0	1	1	1	3	1	3	4	0	1	1	0	2	5	5	4	1	5	0	4	19	3	X16869	94.6	479	1	1153	1696
20	00019	00019	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
21	00020	00020	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	W31469	97.9	334	1	319	651
		00021																																	

Table 1

DOCID: <EP 0679716A1 >

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku
(C) CITY: Tokyo
(E) COUNTRY: JAPAN
(F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS
(D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA
(A) APPLICATION NUMBER: EP 95900295.7

(vi) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: PCT/JP94/01916
(B) FILING DATE: 11. November 1994

DOCID: -EP 0679716A1 -

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SEQ ID NO:7844
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
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SEQ ID NO:7845
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

SEQ ID NO:7846
SEQUENCE LENGTH:38
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

SEQ ID NO:7847
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CCAGGGTTTT CCCAGTCACG AC 22

SEQ ID NO:7848
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
TCACACAGGA AACAGCTATG AC 22

Claims

1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

NSDOCID: <EP___0679716A1_I_>

2. A DNA probe consisting of a purified single-stranded DNA , a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

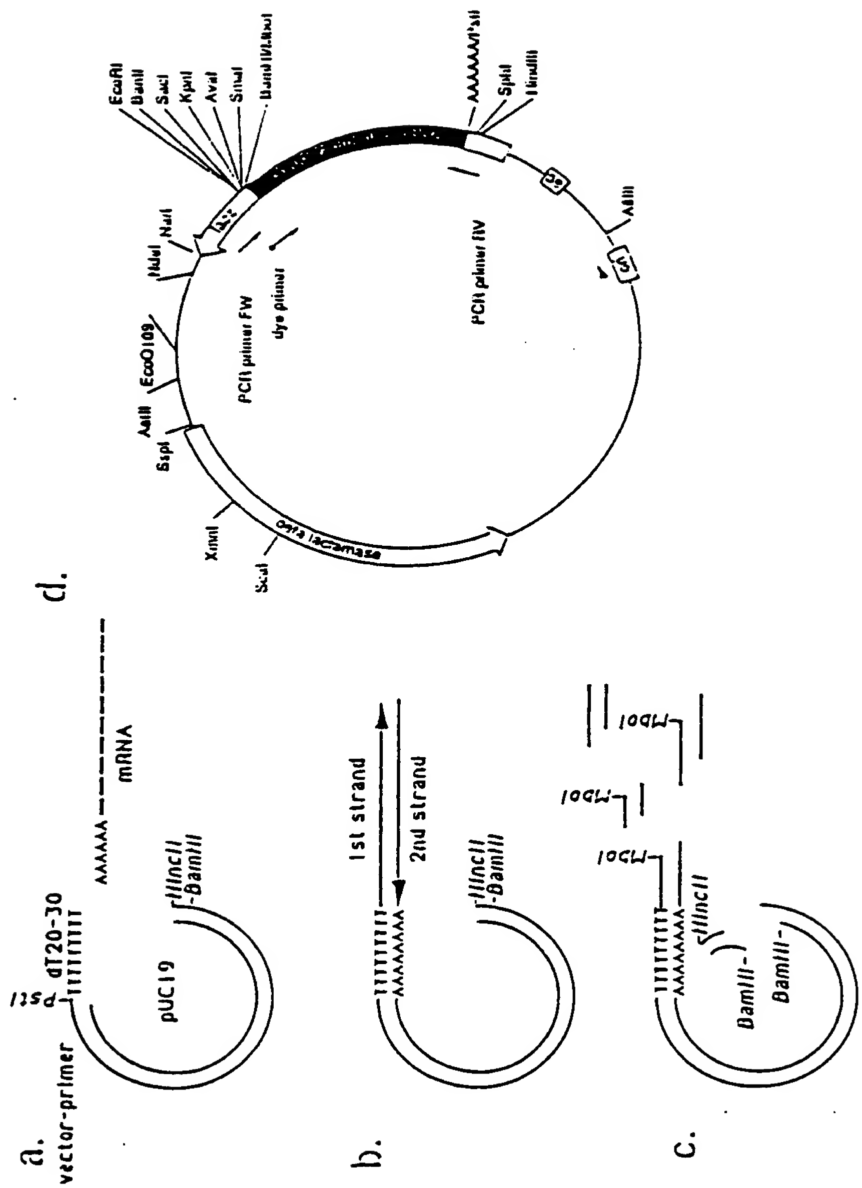
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

Fig. 1


a.
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PstI
dT20-30
pUC19
AAAAAA
mRNA
HincII
BamHI
b.
1st strand
2nd strand
c.
MboI
d.
EcoRI
SacI
KpnI
SmaI
SphI
HindIII
NdeI
NarI
EcoO109
AatII
SspI
XmnI
ScaI
PCR primer FW
dye primer
PCR primer RV

Fig. 2

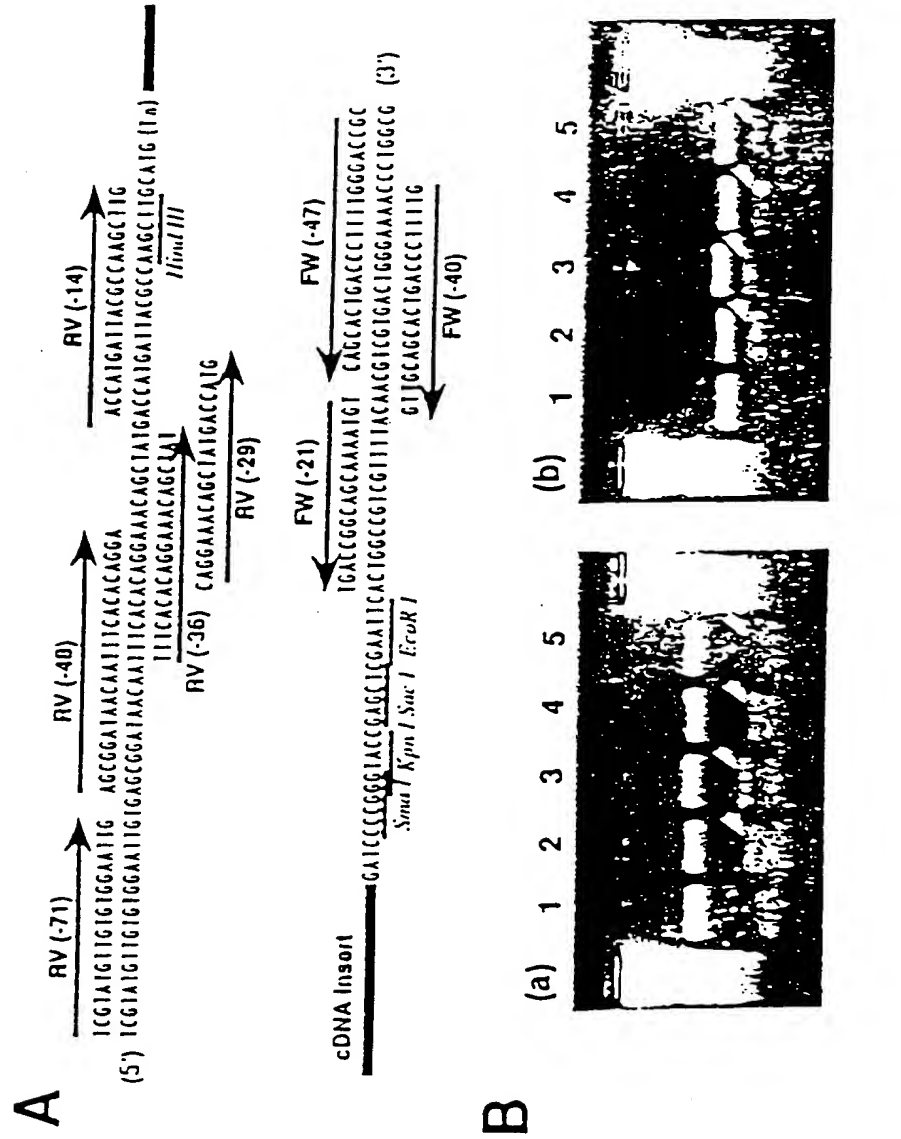
A
RV (-71)
RV (-40)
RV (-14)
RV (-36)
RV (-29)
FW (-21)
FW (-47)
FW (-40)
cDNA insert
(5')
(3')
HindIII
Sma I Kpn I Sac I EcoR I
B
(a)
(b)
1 2 3 4 5

Fig. 3

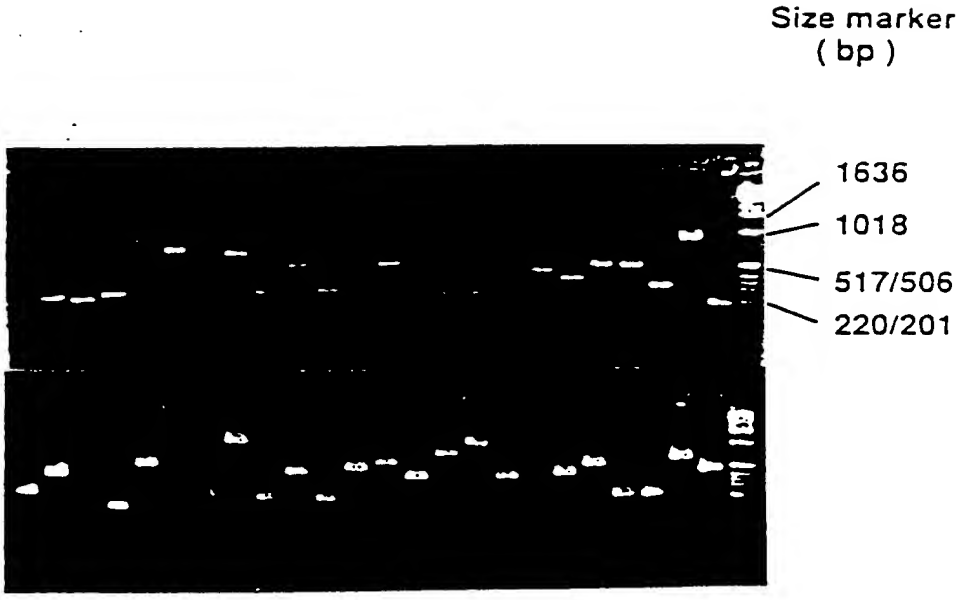

Fig. 4

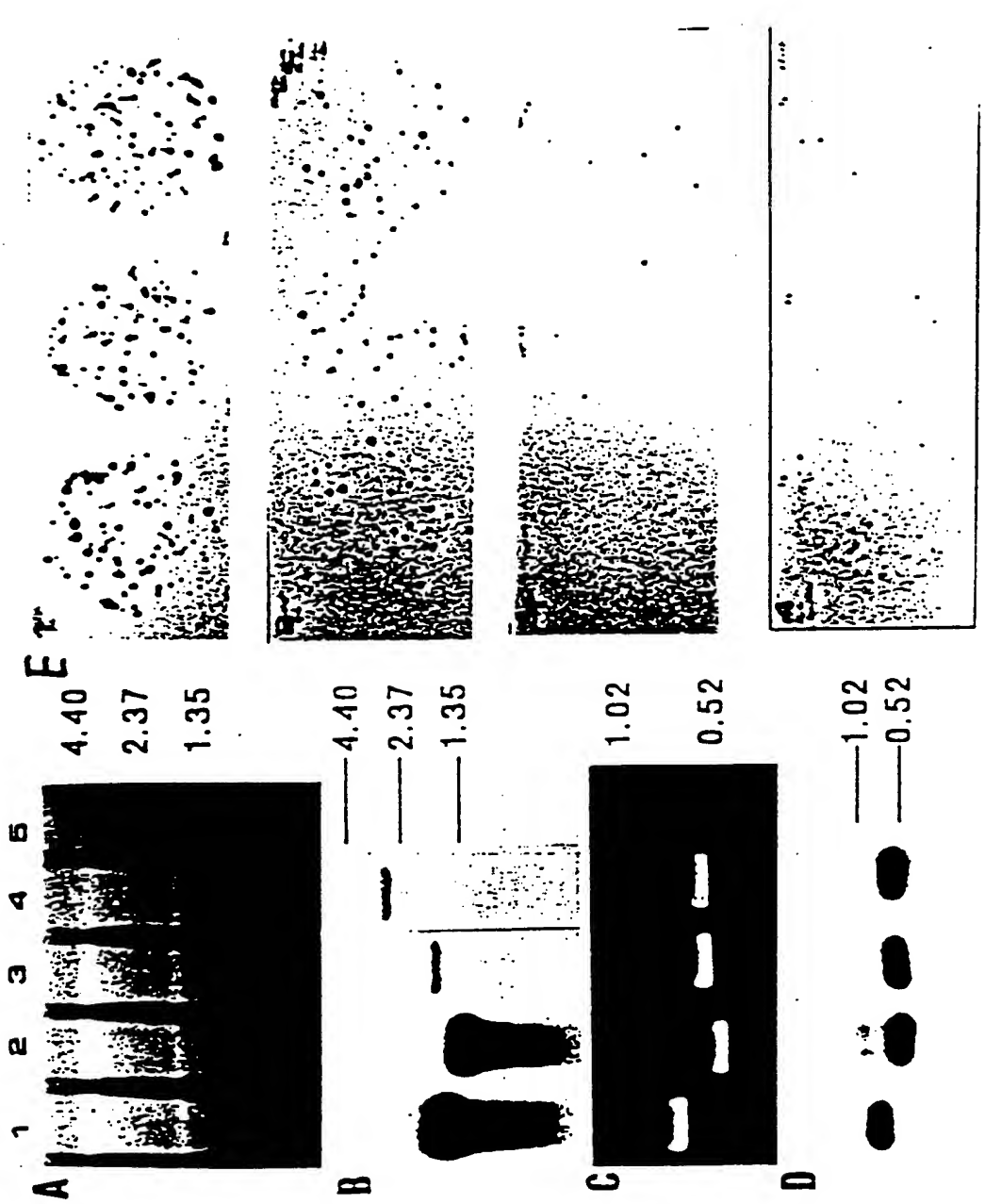

Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1-α	α1-antitrypsin	HnRNP core protein A1	Inter-α-trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b)Band intensity of control blot(cpm)	133	177	100	127
(c)Normalized signal(a)/(b)x10	52	24	1	1.2
(d)Positive signals on colony blot	307	119	7	9
(e)Relative representation	44	17	1	1.3

DOCID: <EP 0679716A1 >

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A in 982 (%)	B "in 8,800 (%)"	C "in 26,400 (%)"
I	a15	Elongation factor - 1Aα	22 (2.2)	307 (3.5)	NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT
	lb038	α-1-antitrypsin	8 (0.8)	119 (1.4)	NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)	27 (0.3)	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT
II	s155	unknown	1	2	5 (0.02)
	s159	unknown	1	2	4 (0.02)
	s639	unknown	1	1	3 (0.01)
	s635	unknown	1	0	2 (0.01)
	s170	unknown	1	0	1 (0.004)
	s154	unknown	1	0	1 (0.004)
	s167	unknown	1	0	1 (0.004)
	s645	unknown	1	0	1 (0.004)
	s647	unknown	1	0	0 (<0.004)
	s632	unknown	1	0	0 (<0.004)

Fig. 5

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EDOCID: <EP 0679716A1 I ~

GS	Cll	Chromosomal position	Sequences of primers		AT	HO	HE	MO	CO	G	T
			Sense	Anti-sense							
gs000788	pm2366	1	CAGAGCCCCAGTACAACTAT	AAGTTTATTGTTGGGGTCAG	48	114	115	104	110	1	2
gs001026	pm2444	1	AATGGGACAGTTACACTTGA	CCAGCTTCCTTGACTTGAGA	48	83	81	>200	>200	1	1
gs001075	pm0883	1	TGGACTGTGGATACCTATCT	ACAAGTACCCCTGAATGGCT	48	124	124	103	107	4	4
gs001087	pm1772	1	GTCACTCTCAGCCATAGCAC	ACCATCTTCAGCCCACACTT	50	104	104	180	>200	6	6
gs001094	pm0347	1	GCCCCTAACACGAGGAACTC	TAATTTCCCACTCCCGTAAC	51	114	116	>200	200	1	1
gs001116	pm1771	1	GGGTTTTCAATAGGGTGTAGACC	GCCCCAATCTGTCAAAACTG	49	95	95	78	107	1	1
gs001191	pm0609	1	TTGCTGGATTGTAACTTTTG	GGCTGAACATTCACTCTTTG	47	97	97	-	200	1	1
gs001200	pm1351	1	TTAAGAAGACCCTTATGGAGACC	AATAATCTTGGTTAGTCACTTAC	47	97	98	-	-	1	1
gs001346	pm0982	1	TCAGGTCTGCTTGGAGGATG	AACTCACAGCACAGTATTTG	53	120	122	>200	>200	1	1
gs001446	pm1518	1	AAGGTGTACAGGATATTTGCAGA	TGCAATAGCCCAATCTCATT	47	130	125	>200	>200	1	1
gs001464	pm1439	1	CCAAAGACCTCCGTTGAACA	TTTGGGAGAGCCATAGACAG	51	100	100	>200	-	1	1
gs001468	pm0427	1	TACTCAGTGGAAAGATAAAC	CAGTGGACCACATTTTCTTA	40	98	98	-	-	2	2
gs001521	pm2785	1	CCCAAATCAAATTGTTAAATG	TTTGAATCAGAGACATGAAGTT	43	102,175	100	>200	>200	1	1
gs001554	pm2291	1	CCAGAGAGTTCAAGGGATTG	GGTACAAAGTGCAAATGACT	46	57	57	78	155	1	1
gs001572	pm2006	1	CCAACATGGTCCTAGCACTG	AAACTTTATTGCAGCTTCTT	44	58	59	>200	>200	4	4
gs000120	pm1350	2	CATGATACTCTTCGGTGGTA	AAACAGTAGTTGCCAGCATT	46	84	109	-	-	1	1
gs001036	pm1730	2	AGGCTGAAATGTGGCATGCT	CCCGTTATTGCTACATGTCT	48	119	119	93	115	1	1
gs001081	pm0931	2	AAAGCAATACAAAATACCAA	TTCAATATGTTTAACCAGTA	40	90	90	-	-	1	1
gs001090	pm0925	2	TAATGTACCACGATGAATAG	TAATGTAATAATGCAGGTAA	45	88	88	-	-	1	1
gs001213	pm2010	2	CCAGATGGAAAGGGAAGTCT	CTGGAATATGGAGAATCAAACAG	47	125	125	150	>200	1	1
gs001252	pm0935	2	TCGAGTTTTGTCTCTAATAA	GGAAATAATCGCTTCAGTTG	43	103	103	-	-	1	1
gs001268	pm2093	2	AGTCCTTCTTGGCTCCTCAT	TATCGTCAGTGCCTTTATTG	52	137	137	>200	-	1	1
gs001438	pm2435	2	TTTTGTACCTACGTAAGAGTACTT	ATCCGTGCCACACATAGTGA	45	105	108	-	-	1	2
gs001442	pm1671	2	TTATTAGGGAGTCATTATTCTGTG	AGTTCCCATTCTTCCACATG	45	67	65	>200	>200	1	2
gs001453	pm1245	2	TTGCTTTCCCGTCTCTAAGT	ATGTACAATTTGCGTATGTAGG	45	75	75	170	190	1	1
gs001535	pm1246	2	ATCTACTGTTTGTTGAAGTG	ACTGATTTTGGTCCCATCTG	44	68	67	-	-	1	1
gs000875	pm0449	3	CGAACATTTCACCTCTCATA	ATGATTTATTTAGGCAGGAA	43	68	69	-	-	3	6
gs001001	pm1758	3	TCTGGCTCTTTGGTGTTGGA	GGCCCACTGAGTACAATGTC	51	115	115	-	-	1	1
gs001218	pm2434	3	AAAGAAAGCACACTGCCTAA	ATGTATAGACAAATCCAAAG	42	90	90	-	-	1	1
gs001219	pm0668	3	GTAGTCTCCTGCCCTTTAGC	AAGGATTTGATTTTCTACAT	43	77	77	-	-	1	1
gs001277	pm1729	3	GGTCCTGTTTATTTGACAT	AAACAAGAGGATGGTTCAGA	43	75	75	155	>200	1	1
gs001306	pm1822	3	GATCCTTGGTGTGTAGTTCAGTC	CTGCAAAATACAGGGAATCAT	46	83	83	160	140	1	1
gs001418	pm2209	3	ACCCCAGTCCCAAATCCAGT	ACACTCCCCCAGCCCTTACT	55	105	105	113	>200	1	1
gs001466	pm2455	3	ATCTAGCTGGCTGTAGTATT	TTAAAGAGATGAATTTATTGGT	42	130	130	190	>200	1	1
gs000271	pm1252	4	GTCCTTTGCTATCTGTGTTA	AAGCATTTATTTGAGGTTTA	43	90	90	95	>200	1	3

Fig. 6

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Fig. 7

gi000448	pm2256	4	GGCCAAGTTTCTTCTAGTAT	GTTCAGTTTTATTCAGAGCA	42	62	62	>200	69	1	2
gi001052	pm1151	4	GTGCCATGCACTGTTGTTAT	GTCATATATTCCATCATCAA	43	80	80	-	-	1	1
gi001215	pm0988	4	AGAAAATTAATAGCATAGGT	TAGAGTCAAAGTTGCCTGTG	43	100	100	130	-	1	1
gi001298	pm2367	4	ATCAAAGTTTAATTGCTTCA	CATCCCATCACATACAAGTC	43	116	116	>200	180	1	1
gi000993	pm0904	5	TCTCGTGAAGAGCAGCACAA	TCTAAAGGAAGAACAGCATC	49	101	102	113	200	1	1
gi000698	pm1809	5	AAGCAATGCCTTATCCACAG	CTAAAGAGCTTGAACCCTTCAT	45	87	87	>200	>200	1	1
gi001065	pm0319	5	TCACCCAGATAATTTACAGT	GAGACATAAGCAGGTAAGAT	44	120	120	-	-	1	1
gi001101	pm2364	5	TTACCTTACCGTGTCTTTAC	AGACAAATATCCCAAAAAGC	47	89	89	100	>200	1	1
gi001461	pm1160	5	ATTTTGTGAGTGGTTTACTA	AGAAATGGATGCTTTTATTC	43	101	99	>200	>200	1	1
gi000053	pm2720	6	AATGTCATAGTCTCCTTTCA	TGCATCCTTCAATGTCTTCT	44	78	78	72	>200	2	3
gi001326	pm1154	6	CATTGAGACAGCAGCAACAG	CCTGGCCCTCTTCCTGAGTA	53	102	104	145	200	1	1
gi001434	pm1216	6	TAGGCAAAACACGAGAAGAG	AAGGAGCTGGTGTCAGGTTC	48	65	65	110	>200	1	1
gi001457	pm1785	6	TATATGCAAATATTCCAAAGTCTG	TCTAATAATTCTGGTCCCTTATCT	46	90,>200	90	>200	>200	1	1
gi001523	pm0285	6	TTGTAACGTGTGTCGTCAGT	TTTAAAAATGTCATGGTAAT	42	86	70	>200	100	1	1
gi001525	pm0328	6	GCACCTAAGCCTCCCAAAGT	TTTTATATCAGTCCAAGAGC	49	138	138	>200	>200	1	1
gi001562	pm2619	6	TCTGCATTGACAAGGACCAC	TTTGAGATTTTAATGAGTCATTC	43	62	62	>200	45	1	1
gi000624	pm0991	7	GACCTGAAGTGTGAATGAGT	AACTTAGCTTTATGGGATTT	45	119	119	>200	-	1	2
gi001145	pm0281	7	AGCCAAACTCGGGGTCATCT	CCACGGGACAGGTGAGTCAT	56	159	159	115	>200	4	4
gi001469	pm0219	7	AATCATTTGGCGAGACTGTA	AAGACAACTTTATCCAGACA	45	88	85	130	-	1	1
gi001579	pm1102	7	TCAGGCAGTCTGCTCAGATA	TTTGCAGGTTAATCTGTTTA	44	77	76	170	-	1	1
gi001207	pm0956	8	AACAGTATTGCGTTGTCAGACTAG	TCCATTAATAAGGCCAGTCTTCAG	47	81	81	105	70	1	1
gi001176	pm2527	9	TTGCCTCTAATGGTGTCTAC	AAAAACCAGAACACACTAAG	48	99	99	118	180	1	1
gi001248	pm2708	9	TGTATTGGATTTGGATTCTC	CAAAAGCAAAACAGCAGATA	44	95	95	-	85	1	1
gi000260	pm0995	07	TTGCCATCAAAACACATACA	CTTGTGAGTTTTGGTTTCTG	43	55	55	-	-	1	1
gi001055	pm0959	07	TTAAAGAATCACCCTCATTG	CACATGCTTATTGGAACACT	44	74	74	72	73	1	1
gi001157	pm0547	10	AAGTATTGTGCAAAGATGTA	AAGAAAACACTGCCTTGTGG	45	138	139	>200	>200	2	3
gi001268	pm2245	10	TGTGAAATGCTATCTCTCCT	GCAATCGTTCCATATCAGT	47	100	100	200	>200	1	1
gi000228	pm2664	11	ATCAAAACAAACAATCCAGA	ACTATAATATACTGCCAACT	42	117	121	134	95	2	2
gi001159	pm0880	11	GAATAGCTTGGAGATTTCAC	GGAGAATCATACCTTCAGCA	46	100	100	84	95	1	1
gi001315	pm0445	11	AAAGTGACCTTGATGGACAGTGGA	TCGAGCCAAAAATACATGCTGACT	50	153	153	>200	160	1	2
gi001352	pm2943	11	AGGGTGAAGGGTATTTTACG	CACATCATGGTTGAGAGCTA	47	83	85	-	-	2	2
gi001469	pm0559	11	AACCCTCTAGTAAGGCATTG	TTATTAAACCAAATCCAGTA	37	47	47	125	53	1	1
gi001570	pm2810	11	CTGTAAAGGTTTTTGGAATTATGT	TTTCATTTTTCTACCAGATTTATT	42	75,82	75	145	>200	3	3
gi000279	pm0266	12	AGTGTATGGAAGACCTTGAG	GTTCATTGAAACGGTGTAGC	48	130	130	103	>200	1	2
gi001163	pm2756	12	TCTCCCTATTCACAACCAGT	AATGATTTCGTAGGATAGCA	49	88	89	>200	120	1	2
gi001193	pm1193	12	CACAGCATAAAAGAATCATA	ACCCTAAATTAGTTTCTCAC	46	100	100	-	-	1	1
gi001235	pm2790	12	CATCATGGTACAGTCAGAAG	CAGTTTGTCAAAATGTATTG	44	83	82	93	87	1	1
gi001274	pm1355	12	AGATGTCAGTATTCTCCTCATGG	GAGAACAGCAGTAAAGCAACCAC	47	87	87	>200	>200	1	1
gi001308	pm0368	12	CCAAAGTGCTAGGGTTACAG	TTCAATAGACCTTGGGTTAC	47	95,165	95	>200	>200	1	1
gi000159	pm2645	13	CTAAGATTTAATGCGATTCC	AGTTAGTGTATGGCAGAGGA	46	104	104	>200	-	1	2

Fig. 8

gs001044	pm1659	13	TTGTAAGCCTATCAGAGTCA	AGACAGACTTATGCCATCTA	44	109,200	109	>200	100	1	1
gs001290	pm1731	13	GCTTCTTCCTGTGCTGTGGT	GCAGTTAATCATGGCTATTCTCC	50	122	122	>200	190	1	1
gs001362	pm0118	13	ACTGAAATGGAACATAGTCT	TACATTACATGACATTGTGA	40	61	61	95	103	1	1
gs001366	pm0364	13	TGCTTAGCTTTCCCTCCTTA	GAGCATTTCTGTTGTTCCTA	45	67	67	.	.	1	1
gs001389	pm2301	13	CATGAACCTGCTCACGACAA	GCCTTACTTTAATGCTGACC	51	100	100	100,>200	.	1	1
gs001492	pm0541	13	AAATGAATGTAAATAGCACT	ATTTAGTTTACAGGGAGAAT	41	72	72	.	74	1	1
gs001367	pm0441	14	GTTTTAAGTTTTGATTTGGG	CATTCCACTCTTACATTTCT	41	77	77	>200	180	3	4
gs001564	pm2307	14	CGTTCCTAAACTCTGAAATC	AATGCTCATTTATTCTCAAG	42	55	55	>200	>200	1	1
gs001576	pm2019	14	ATCACAATTACCTTTAGTTG	ACGATAACTTTATTGGAGAT	39	69	69	.	.	1	1
gs001339	pm2220	15	TCCCCATCCTCAGTTGAAGT	TGAGAACAAAAGGAACCAGT	47	70	70	80	150	1	1
gs000980	pm0985	16	TTGGAATGGAACCCTTGCTA	ACTTATGCTGCCTGAAATGG	48	79	79	66	70	2	2
gs001242	pm1127	16	CCCTTGTTTTTACATGTTCA	TATTAAATTCTCCCATTCAT	44	105	105	103	102	2	2
gs001516	pm2543	16	ACAGTGCTAAAATCAAAGGTG	TCTGACAACTCAAGGTGCAAT	45	70	70	>200	.	1	1
gs001566	pm0913	16	TTTGTGTCGGACTATGTAAT	TCACTTTTAATGGGAACCAG	41	53	53	>200	>200	1	1
gs000806	pm1157	17	CTCTCCATGTTCTCTACAAG	TAGAAGGAGAATCTGTGGTT	47	77	77	140	>200	2	3
gs001015	pm2369	17	ATATTCACCTTCCCATCCAT	TCAAATACGTCCTCTCAAGC	50	80	80	>200	>200	1	1
gs001156	pm0202	17	CAGAAATTAAGTGCAGCAAT	TCGTATCTGCATCTTTAAGT	45	103	100	>200	>200	2	2
gs001173	pm2117	17	AAAATCTTGTGGTTATTTCC	GTGATTCTACTGTACATTGC	41	118	118	145	200	1	1
gs001301	pm1878	17	TAAATTTGTGGAAATCTCTTGGA	ACACATTTGGGTTTGCTTTAAC	47	100	100	95	97	1	1
gs001316	pm0514	17	TGTGACAGCAGCAGCTTCAT	TCGTACATTTTAATTCCACC	45	128	129	.	1	1	1
gs001356	pm0538	17	CATCTCACAGACAAGGAAAC	ACCTAAGAGTCCAGAGAAAC	40	90	90	69	>200	1	1
gs001495	pm2212	17	TGACTGCAATAAGGAGTTGT	GAACATACCACGTTTATTTCT	46	90	90	180	>200	1	1
gs001522	pm0642	17	GTCTTCAGCAGATTTCAGGT	ACTTTCTTCTTGAGGACACA	45	68	68	160	.	1	1
gs001078	pm1815	19	TGTGTTCTCCAGCTTTGTAG	GTTACATTGCCTTGGTACAG	49	65	65	>200	>200	1	1
gs001117	pm0289	19	GGATCAGACCAACAGTGCTG	GCAAGGTATAAAACAGATTA	46	50	50	.	.	1	1
gs001467	pm1688	19	GAAGCCCACCCTGCACCTCA	GGAGAGTATTGGGGAACGGT	54	93	93	>200	>200	2	2
gs001069	pm1879	20	GCCATGCTTGTAAAGTGATGT	TTAAGAAGCCATTAGCTAGGATA	48	140	140	.	.	1	1
gs001088	pm1146	20	GCCCTTAGGATTCACTGCTC	ACCACCCAAGGTCTTTCAGG	52	66	66	180	>200	1	1
gs001069	pm0112	20	TGCTGGATGACTTCTACACG	TCCCTATCATGGCTGCTGTT	49	59	59	59,115	59	1	1
gs001128	pm0332	20	CTGCTCGGCTAGTCTGACTC	CAAATGGTCTAAGAGGACAT	49	135	135	153	160	1	1
gs001132	pm0647	20	TCTGAATGATGATGGAAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	.	.	1	1
gs001158	pm1774	20	GGAGCCACATGGATTGATTG	AAATGTACCCCTGGCACCTC	52	124	124	>200	>200	1	1
gs001210	pm1235	20	AGCCATCTGGTTATGTCTTA	GGAGCAGAATGAAACTTCAC	44	90	90	>200	>200	1	1
gs001377	pm1701	20	TCCATGGTGTTAGAAGCCAG	CCACATCTCCAACAGGGAGT	54	142	142	>200	74	1	1
gs001395	pm2101	21	GTCAGCTCAATGCTACACAG	TTTATAGTGCAACACAGAGT	45	130	130	180	>200	1	2
gs001427	pm0648	21	CTTCTGCTATAAAAGTAGAG	ACAATTGGTTCACTAAATGA	39	50	50	145	>200	1	1
gs000378	pm0912	22	GGTGTAGTGTAACCATTTAG	AGTTGCACCCATCTCCTGTC	46	124	124	>200	>200	1	1
gs001444	pm0911	22	GGTCTTGTTCTCCCATCTGT	AGAAAGCCCCAAAGTAGTCC	40	65,80	65	100	125	1	2
gs001473	pm2231	22	TGAGCTGCACTTACCTGTGAGAG	AAGCAGGTTGAGTTGGGTTTTCT	50	94	94	67	135	2	4
gs001479	pm2328	22	TACAGCCCTCCCAGCTAAAC	TTTATTCTGCATCCACTACAA	46	65	65	190	>200	1	1

Fig. 9

gi000999	pm1759	X	CTGCCATAGTTACCTGGATT	TCACCCACCACTATTTAGCA	47	103	103	.	.	1	1
gi001149	pm2180	X	GGAGGGGAGATATAGATTGT	AAAAAAATCCAGAAGACTGA	46	70	70	135	150	1	1
gi001161	pm0608	X	TTCTATAAGTGTGACCAGTT	GGAGGATTTGAGATACACAT	40	85	85	>200	77	1	1
gi001406	pm1294	X	TAATGCCAGTGAATGTTGCGTAA	GTAAAGGTTTATCCTTGCATCAGA	47	82	82	>200	80	2	3
gi001160	pm2289	1,18	ATCCTGCTGAAATACATCTG	GGGGAGAGACATCACATGAC	46	70	70	68	130	1	1
gi001436	pm0113	1,2,12,13,Y	GATCCGATGGGAGTGTAAAT	AATACAAAGCTAAACCACAA	44	69	69	170	.	1	1
gi001404	pm2272	1,2,3,5,8,12,14,17,X	TTGGAATTGACATTCTCTAT	TTTATTGTAACAAAGCAACT	43	130	130	150	132	2	2
gi000803	pm0314	1,2,6,X	TATCAAGCTGAAAATGTCAC	TTACTGAATCCAGCCAACCA	45	93	93	110	.	1	3
gi000140	pm1461	1,3,4,5,8,16	TCCAAATGAAGAAGGTGTTA	AGTTGACAGCCAGGTGAATG	49	96	96	100	100	1	3
gi001354	pm1561	2,20,21,22	GTCTGTCAAGCCAAGATTCA	TTTTTATTGTTGCTCCAAGT	49	110	110	170	150	1	1
gi000336	pm2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATTCTGGACT	TTATATGGTTGTTACACTCG	43	61	61	.	.	2	6
gi001077	pm0943	2,5,14,C	GCCTTGTTATTTCACCACTC	ATCTCCCTTTGCTCCAGTTA	46	82	82	>200	82	1	1
gi001192	pm1853	2,8,12	TCTGAGGACATTCCAAGACAG	CAGTCAAAACCAACACGGTAT	49	95	95	93	160	1	1
gi000213	pm1778	2,9,13,17,X	TGCAATAAAGGGAAAGACCA	CCGTTGTAGGTGATGAAATG	49	78	80	>200	>200	1	2
gi000919	pm0885	20,X	GTCATTTGTATGCAATTTCC	ACATTTTTATTTTTTCAACG	37	45	45	.	.	1	2
gi001109	pm0457	3,10,15	CATGTACTCAGAGGCACTTC	GCAACTACAAATCCCAAACT	50	133	133	>200	150	2	2
gi000071	pm2651	3,4,M	CAGGGACTGGAGCAGGAAAG	GATTTAACCCATTAGGAAGC	50	101	101	101	88	3	3
gi001426	pm2632	3,6	TTAGGAAAATATGGTTAGACAG	ATAGTATTGGGTTGACACAGTA	43	80	80	>200	120	1	1
gi001391	pm1133	3,8	TGGATTTGCTTTACCTTGTT	ACACCCTCAGGAGATGTTAC	47	93	93	95	>200	1	1
gi000377	pm2250	3,9,10,15	GCACTACAAGCCAAATCAGA	CTTCTTAACACCAACAGCAG	50	96	96	>200	125	2	10
gi000605	pm0626	4,6	GGATTTCTATTTGCTGTCAT	GTTTATTGTACGGCATTTAC	44	105	100	>200	>200	2	4
gi001212	pm1234	6,20	GCATTAAACAGGAAACAATA	CTGTCCATGTGGCATAAACC	44	110	110	105	107	1	1
gi001312	pm0606	7,18	AGATGCTAACATTAGGGATA	TTTTAGACATACAGAGGAGT	43	81	81	102	.	1	1
gi001441	pm1253	9,11	CCAGACTACAGGCTGATGGC	CCCTTACCCCAGCAACTCTT	55	75,130	75	>200	>200	1	1
gi001357	pm0115	9,M	ACCAATGTCACTGCTTCTAAAATA	CCCATAATAAGTGAAGAGGTAGTTC	48	125,155	127	125	>200	1	1
gi001261	pm0428	10,15,22	AAGAAATTGTTTACTGGATT	TTATCTGACTTGGAGGAAAT	42	107	107	.	.	1	1
gi001456	pm2420	10,15,22	ACTACCCCTGAGATATTAGTT	TTCATTTATTTGATTAGTTGA	46	100	100	170	.	1	1
gi000250	pm2303	11,M	ATACCACTTCCGCTGTCACG	GAGGAGCGTCTACTGGTCTT	50	72	74	72	>200	3	20
gi000314	pm2643	12,19	GCACCAAGAAGCAGTTCCAG	TTGGGAATGAGAAAATAACT	46	83	83	81	.	1	7
gi000103	pm2773	12,M	GATCTCAGTTCTGCGTTTATT	TACATACAAAGATGCAAACAGT	44	80	80	79	68	1	1
gi001487	pm2725	13,16	ATTCTTGTGTGCTGCTTTCC	GTCTCTCTTCTGATGGCTGA	46	62	60	135	180	1	1
gi000976	pm2780	14,16	AACCTGTTTTACCGCATCTT	AGGTTATTTGTCCACCAGAA	48	87	87	>200	>200	1	1
gi001435	pm1683	17,20,C	TGTTGGTTCACCATTGAGAC	AGAACAACACATCAAAGATGC	46	90	90	>200	90	1	1
gi001393	pm1748	17,22,Y	GAATGTCATCCAAGACGTAG	CTAGTTATATCCTGGCTCTG	44	81	81	>200	200	1	1
gi000056	pm0964	17,C	TTTATCCCAGCAAGCACAAC	TCTTCCTCTTCACTCTCCTC	49	120	120	>200	170	4	11
gi001369	pm2217	17,C	ACTTAAAGTAGCTTTGTACG	TGCCTCCTGGTCTGATAATA	43	95	95	>200	95	1	1
gi001440	pm1213	18,C	CCCCAGTTAAAGATTATTGT	AGTGACGATGGAAGGATGTA	44	92	92	.	92	1	1
gi001217	pm1118	19,20	TGCAGAGTGATTTTCCAGAG	CGTAGGTCATTCTTTTCAGC	46	75	72	160	65	1	1
gi001009	pm2824	19,22	ATCCCTCTGTCTATTCACAC	GCTCGTTTAACTCACTTCAC	46	110	110	130	170	2	2
gi001172	pm0887	19,22	GCCTGCATCTGTGTTGACTT	AACCTCTGGGAACAAATCAT	48	91	89	160	86	1	1

Fig. 10

gi001057	pm2049	C	AGGACACAAACACCAGCTAT	TTTTCTGATTATGACATGAC	45	75	75	101	75	1	1
gi000473	pm1753	M	ATCTCTTTGTAGCCATCCTG	GTTAAAGTGCTGATGCCATT	42	64,100	64	64	>200	1	1
gi001096	pm2236	M	GTAGAGCTGCATTGACTACC	ACAGACAAGGAATAATCATA	42	108,96	110	110	112	1	1
gi001166	pm0506	M	GTCCCACAGTCCAGCCTAAC	GCCACATATTAGAATCCATC	46	74	74	74	>200	1	1
gi001451	pm2354	M	TGTCTTTGTGGACTCTGCCT	TTTAACAGTCAATAAATACATGTT	44	110	110	110	106	1	1
gi000329	pm2492	M,C	GCTAGAAAGAAGGGCACTCA	CTTAACTCGATAGCCAGGTC	46	75	75	75	75	1	1
gi000253	pm2786	M,C	CACAAAACAGCAAACTTCAG	ATGGTTATTTTATCAGATTG	41	83	83	82	83	2	3
gi000285	pm1704	M,C	TCCACCCAGAGAAGCACACT	AATTCATAGGGAATAGGTTC	40	75,130	75	75	75	1	23
gi000302	pm2318	M,C	TCGAGAAGGACAAAATCACC	GAACAGGGTTAGTCCATTCG	48	50	50	58	58	1	1
gi000543	pm1689	M,C	CATGAGGCTACGGAAACAGG	AGGAGTCCGTGGGTCTTGAG	51	84	84	84	84	4	18
gi000675	pm1442	M,C	AAAGCATCTTGAGAGGAACA	GGAGGACTCGCTTGGTCTTA	49	110,>200	110	110	110	1	9
gi000732	pm1452	M,C	GCAGCAGATACCTTTACACC	TGGTTCATTTCAGTTCCTTC	51	102	105	102	102	3	13
gi000995	pm0268	M,C	GAAGCTCTTGTGAGGAAAGT	CAGACCCCATCTTTTATACC	47	79	79	79	79	3	4
gi001016	pm2703	M,C	ACGATATTTATAGTGATGTG	TCAAAACTTTAATATATGCT	40	93	93	91	92	1	1
gi001053	pm1144	M,C	AGATGAGTGTGGGTCAGAGA	CCATTCCTGTCATTCCAGTT	52	135	140	135	135	1	1
gi001127	pm2290	M,C	ACTGGTGATGGAAGGTTACA	CCACACAGTGAGCACCGTCT	47	55	55	55	55	1	1
gi001167	pm1626	M,C	GAGAGCCCTTGCATCCTTTA	CTTCCCTTTGGTCTTTCTGT	49	100	100	100	100	1	1
gi001216	pm2109	M,C	TAGTCAGAGATTCAGTAAGT	ACATGTATTTTGATAGTCTT	42	110	110	110	110	1	2
gi001253	pm1240	M,C	AACTGGTTCCATCAAGACTG	AGTGAATAAACTCTCCACTCC	40	120	120	120	120	1	1
gi001281	pm1131	M,C	ACTTAAAAACCCACCAGCAT	ACAACAGCAGTCAAATAGAA	47	97	97	97	97	1	1
gi001375	pm0952	M,C	AAGAGGAGTTTCCCTGCTCA	ATCATGGCAGATGGCAAGGA	51	89	89	89	150	1	1
gi001356	pm2216	M,C	ATCTGCATGACCTATAATCT	CGTTCTCTTTTATTTGACAT	45	100	108	100	108	1	1
gi001411	pm0958	M,C	ATGGGTTTATCAGGGGTTTC	GAGACCAAAGGCACTTCTTA	47	80	77	80	80	1	1
gi001460	pm2626	M,C	ACATTGAATGGGGATGAGGT	GGACATTTCTAGCCCACAGC	51	75,55	75	75	75	1	2
gi001482	pm1210	M,C	TTGTTGACATTCCTTTTAGAA	CAGTGCCTCTGTACTGAGACA	46	85	85	85	85	1	2
gi001450	pm0109	M,C	GCCCACAGAGACATCATCCT	TCTTAGTAGGTGCTCTGGTG	51	98	98	98	98	1	1
gi000168	pm2042	No product	CAACCAGTTAGCGTGAAAGT	GAAATAATCCTTGTCATCTA	45	87	87	.	.	1	1
gi000850	pm0304	No product	CTTTGGGATATTTTCTTCAT	CCCTCGGGTACTTTTCTATG	43	60	60	62	.	1	2
gi000983	pm0808	No product	AGCCAGCCTCTTTGTATGTG	CTGGATTTGATTTTCATTAG	44	87	87	.	112	1	1
gi001254	pm1673	No product	TGTGGTATGAAAATATCTGA	TTATGAATGAAGACAACACT	43	98	98	163	>200	1	1
gi001365	pm2908	No product	CAGTAGTGTGCTTTGAAATG	TTTATGTGAAATGTGGTTGT	41	63	63	.	150	3	3
gi001373	pm0361	No product	TACAGCCGCTTCTAAAAGTC	TTTGAGCATCAAGGAAATCT	46	82	82	.	>200	1	1
gi001556	pm0849	No product	TACATTCTTCAGACTCATCG	TTTTCAAAACTTTATTCTT	40	86	86	>200	100	1	1
gi001574	pm1284	No product	ATCAGAGCTCAGTTCCTGTAG	ATTTTGCCTCTTGCATGGTC	44	57	57	67	67	2	2
gi001622	pm1606	No product	GATCTTGAGCCTTAACTGGA	TTTGCAGTTCAGCTTTATTC	45	54	54	.	.	1	1
gi001640	pm0852	No product	GATCTCTGTTCCTTTTCACA	TTTATAACAAGACACCATAC	36	45	45	.	.	1	1

Fig. 11

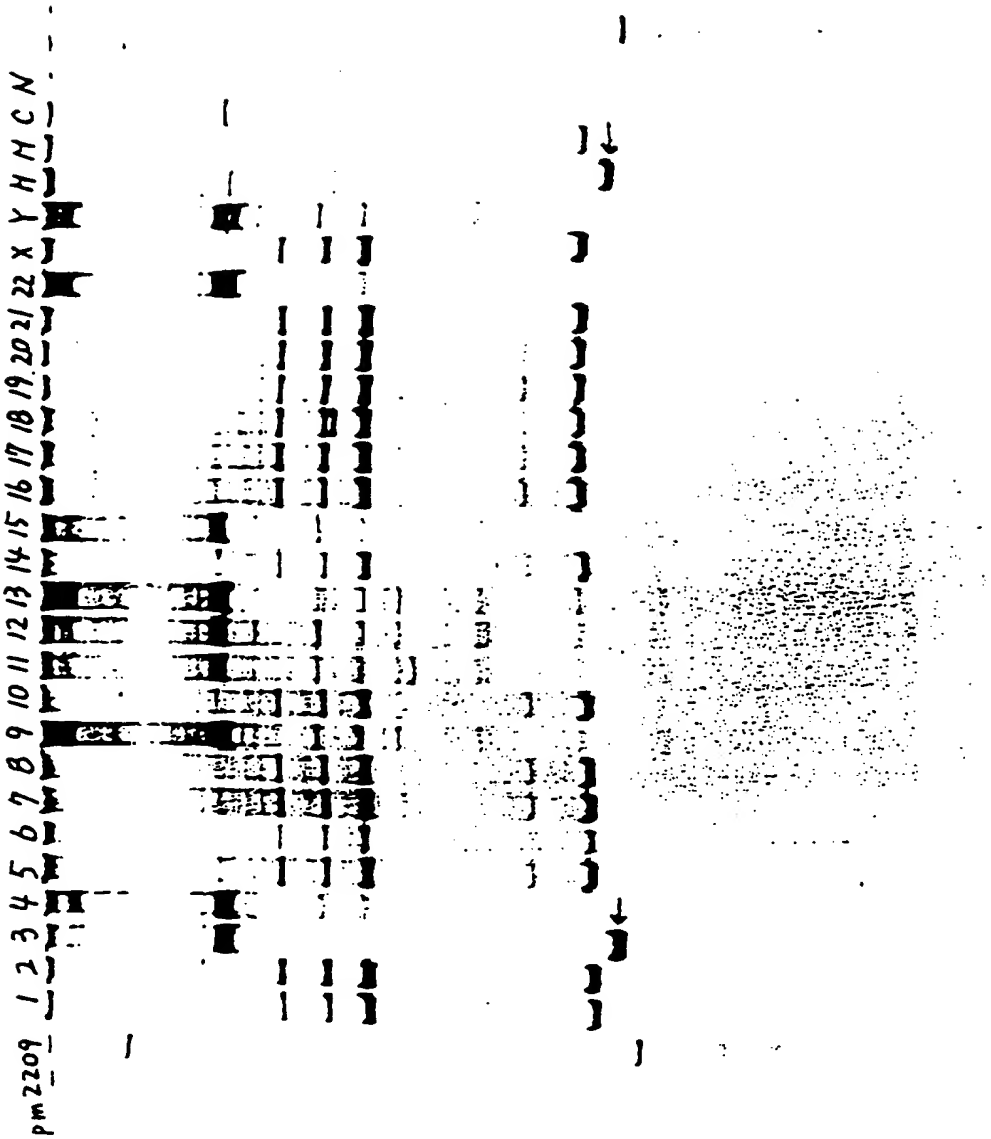


Fig. 12

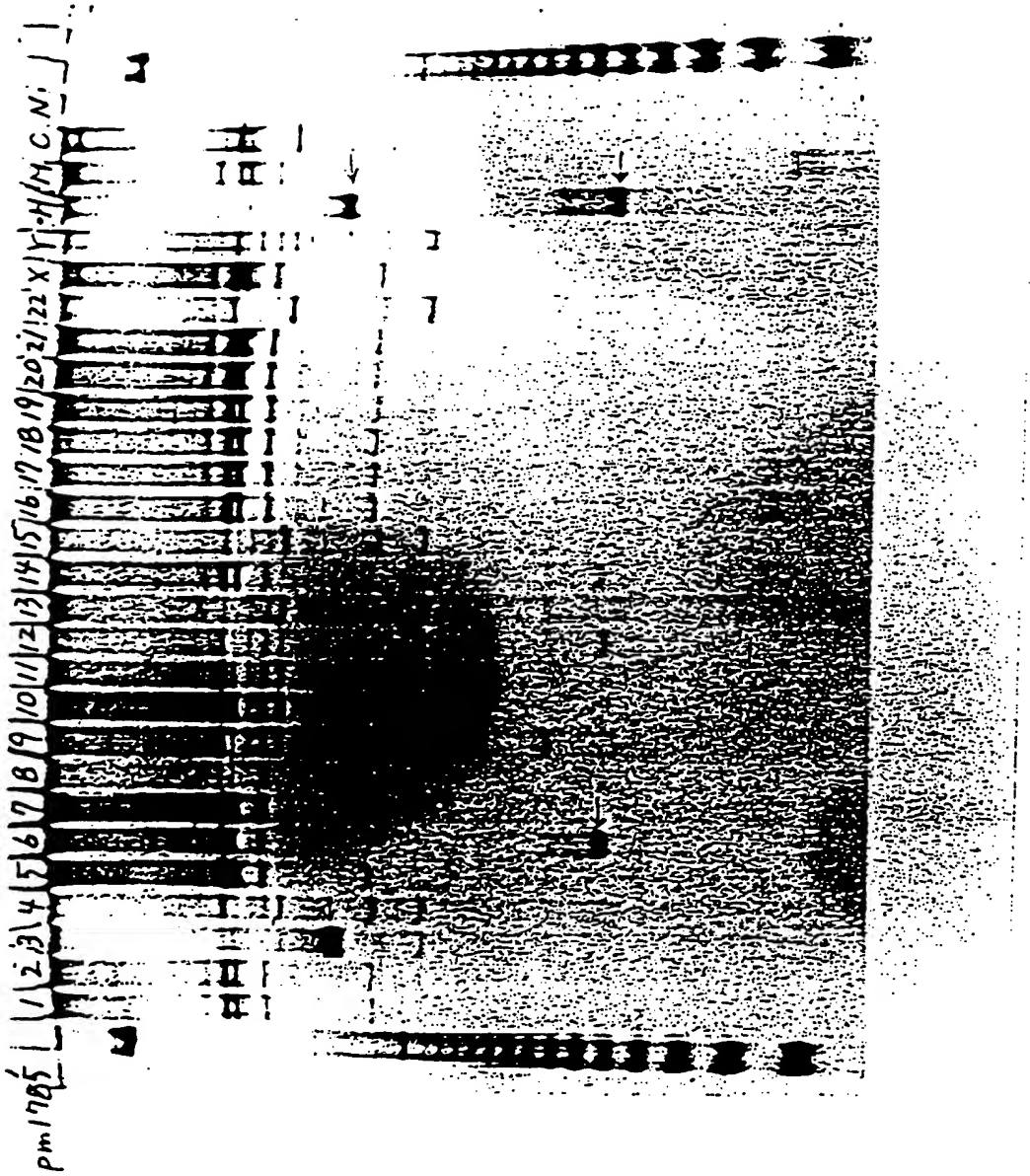


Fig. 13

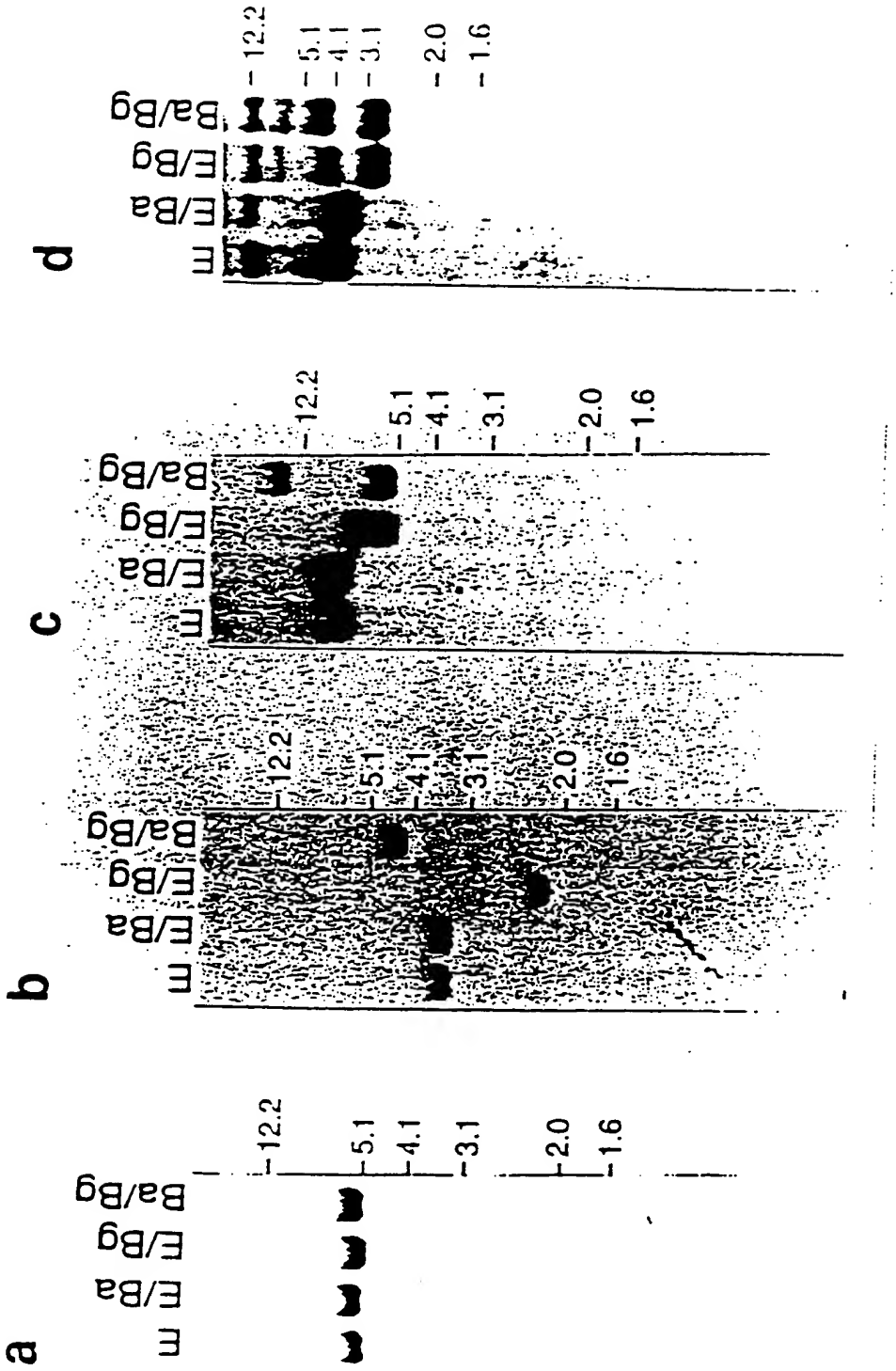
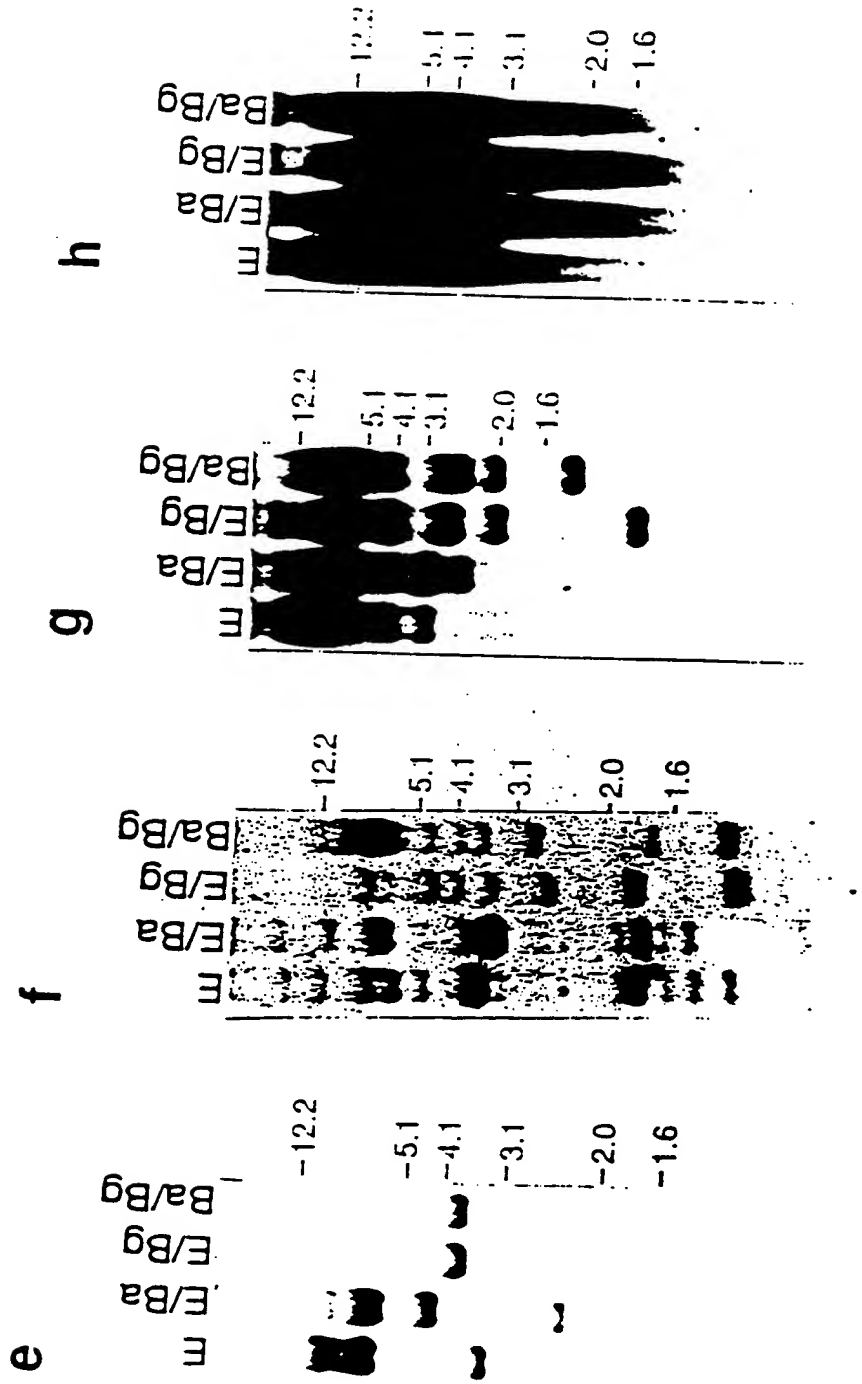


Fig. 14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-3.1
-2.0
-1.6
e
E
E/Ba
E/Bg
Ba/Bg
-12.2
-5.1
-4.1
-3.1
-2.0
-1.6

Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A *	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868 *	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418 *	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

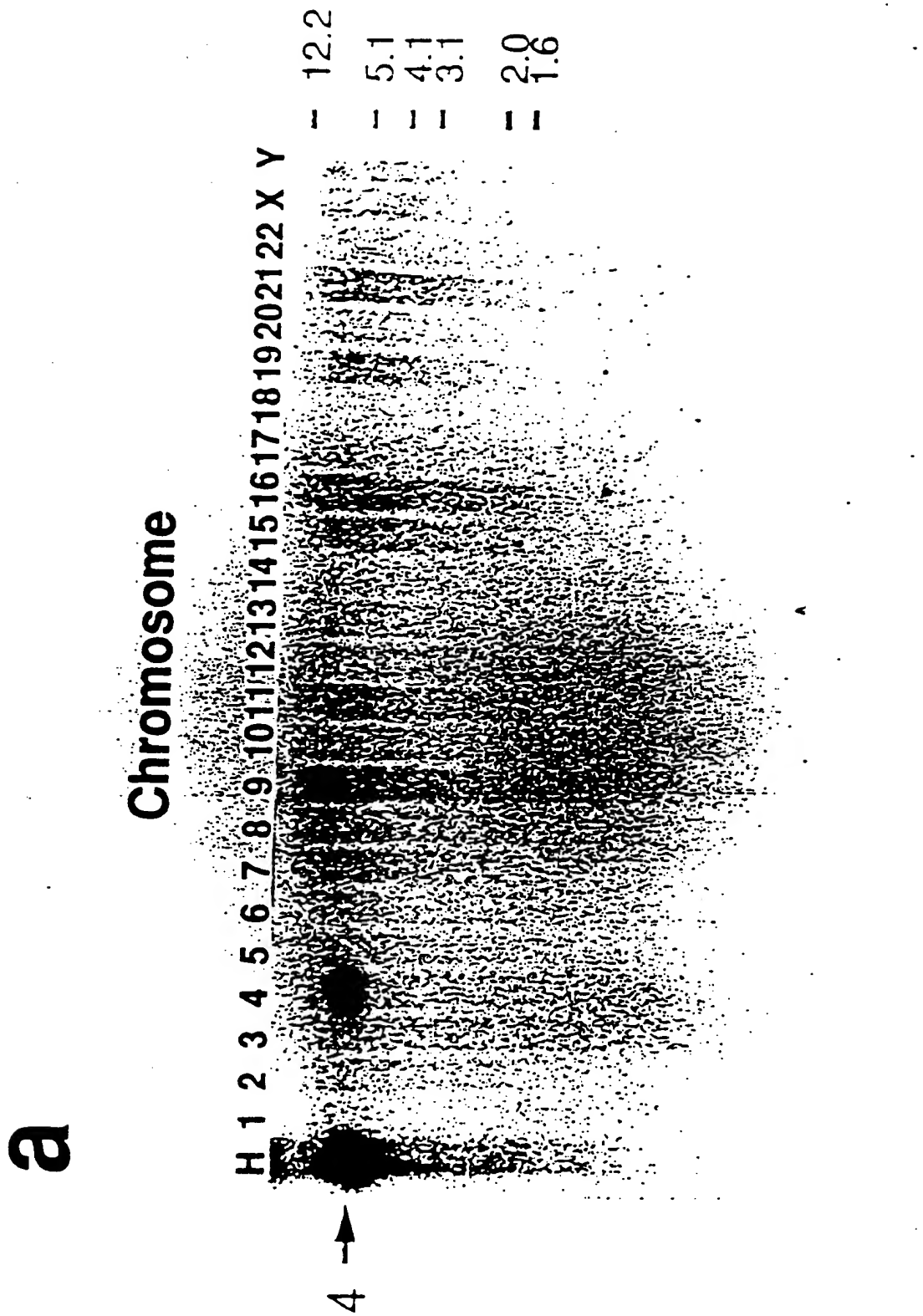
a
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
Chromosome
12.2
5.1
4.1
3.1
2.0
1.6
4

Fig. 17

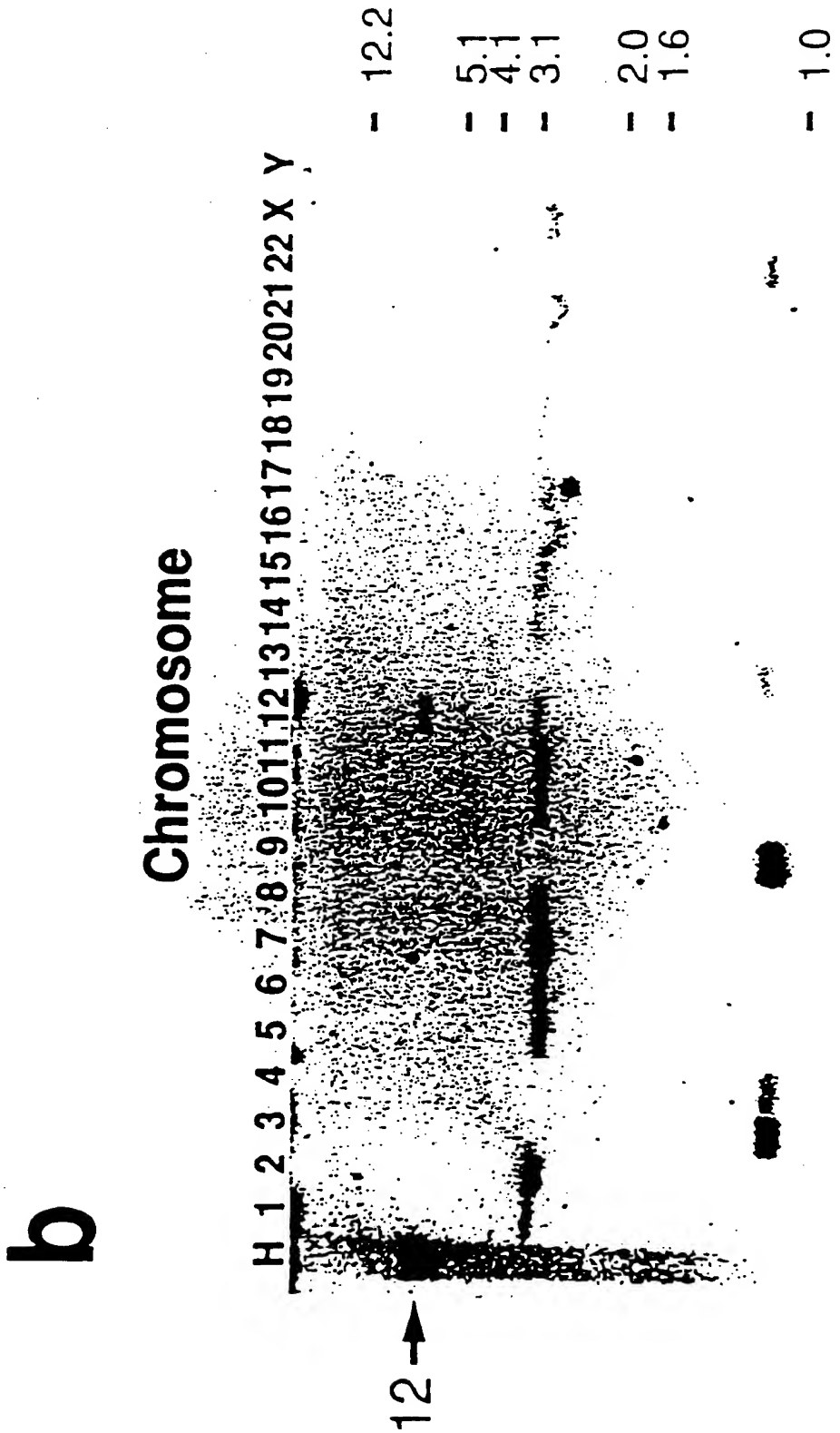
b
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
Chromosome
12
12.2
5.1
4.1
3.1
2.0
1.6
1.0

Fig. 18

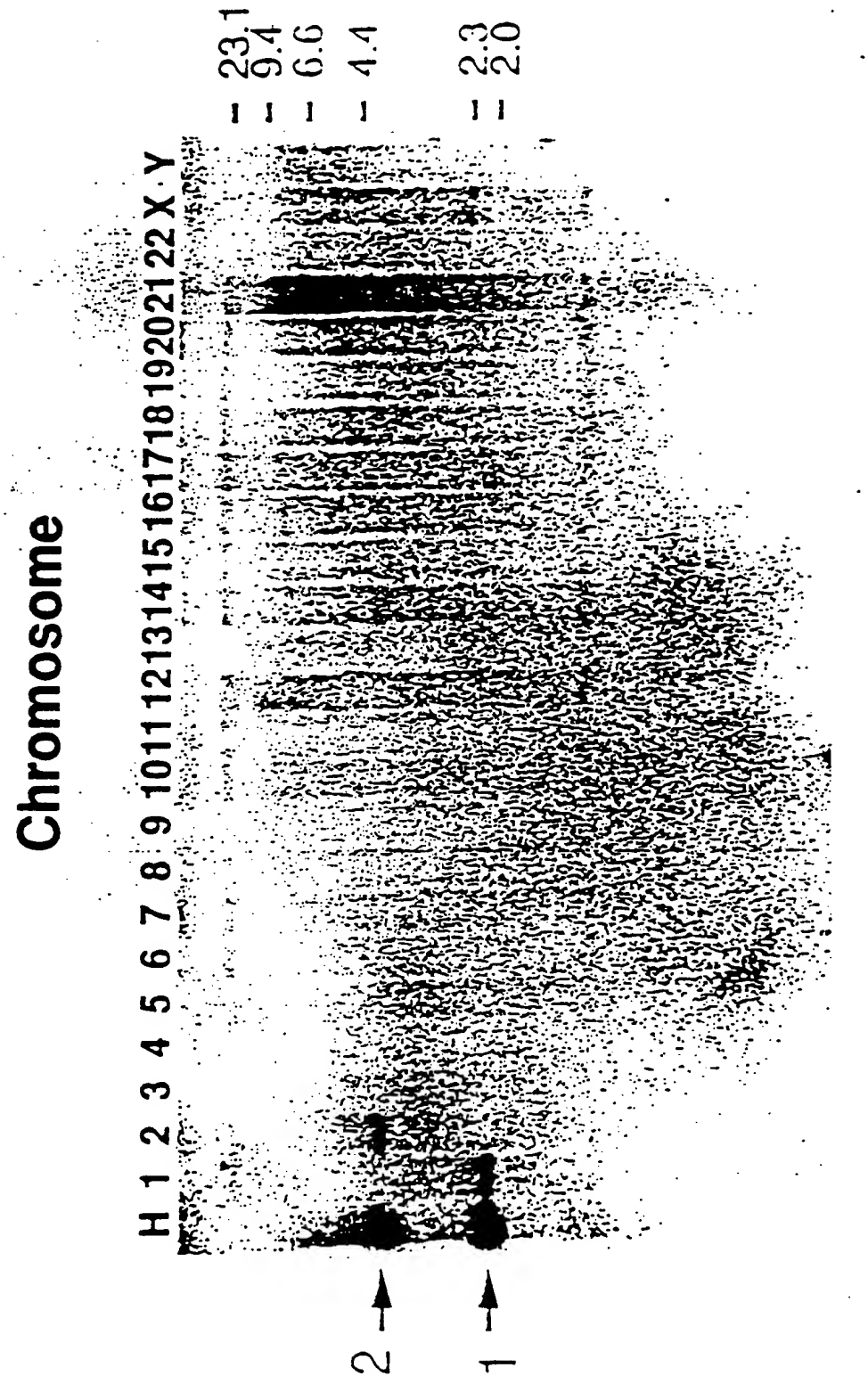
C
Chromosome
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
23.1
9.4
6.6
4.4
2.3
2.0
2
1

Fig. 19

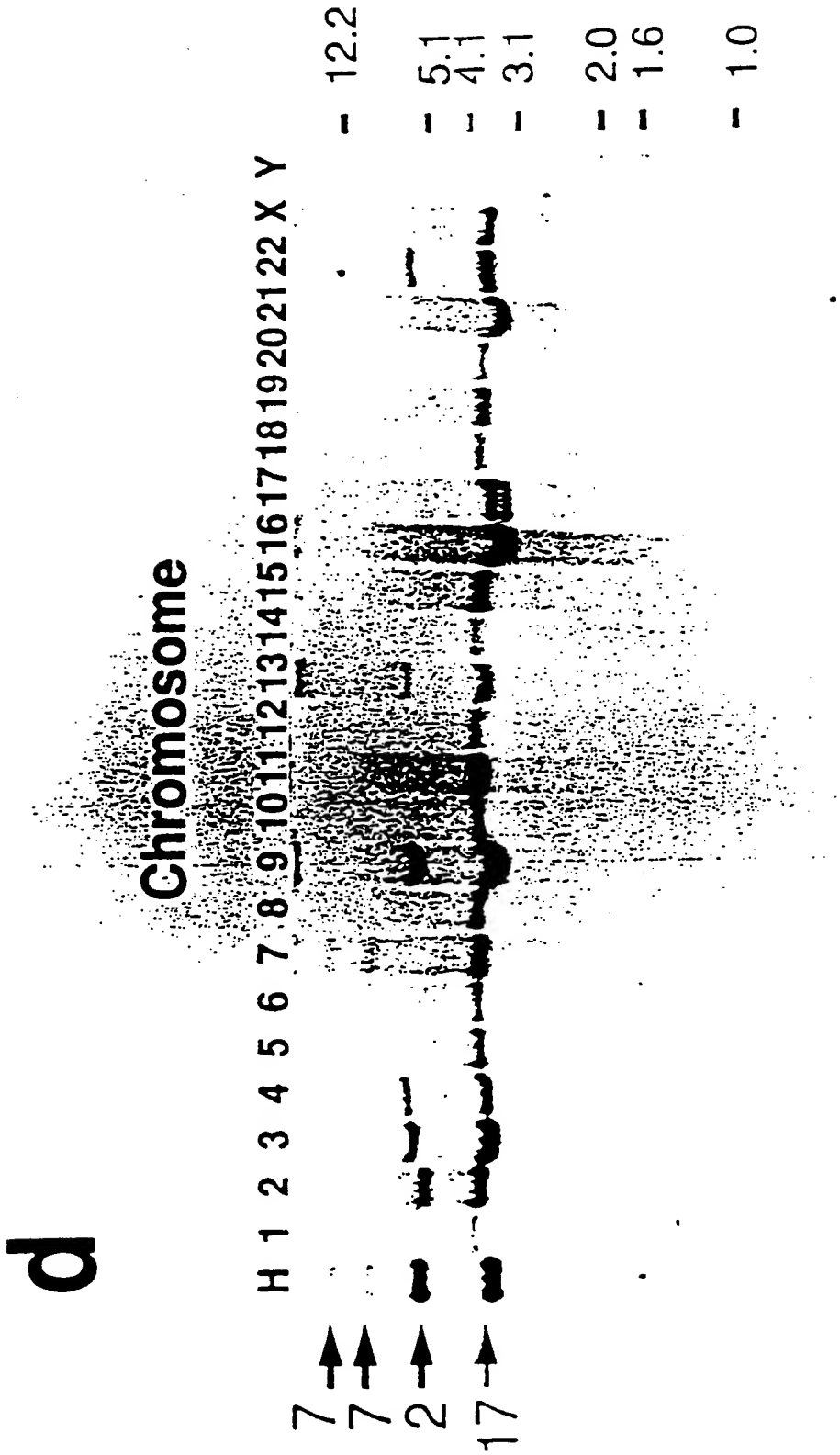
d
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
Chromosome
12.2
5.1
4.1
3.1
2.0
1.6
1.0
7
7
2
17

Fig. 20

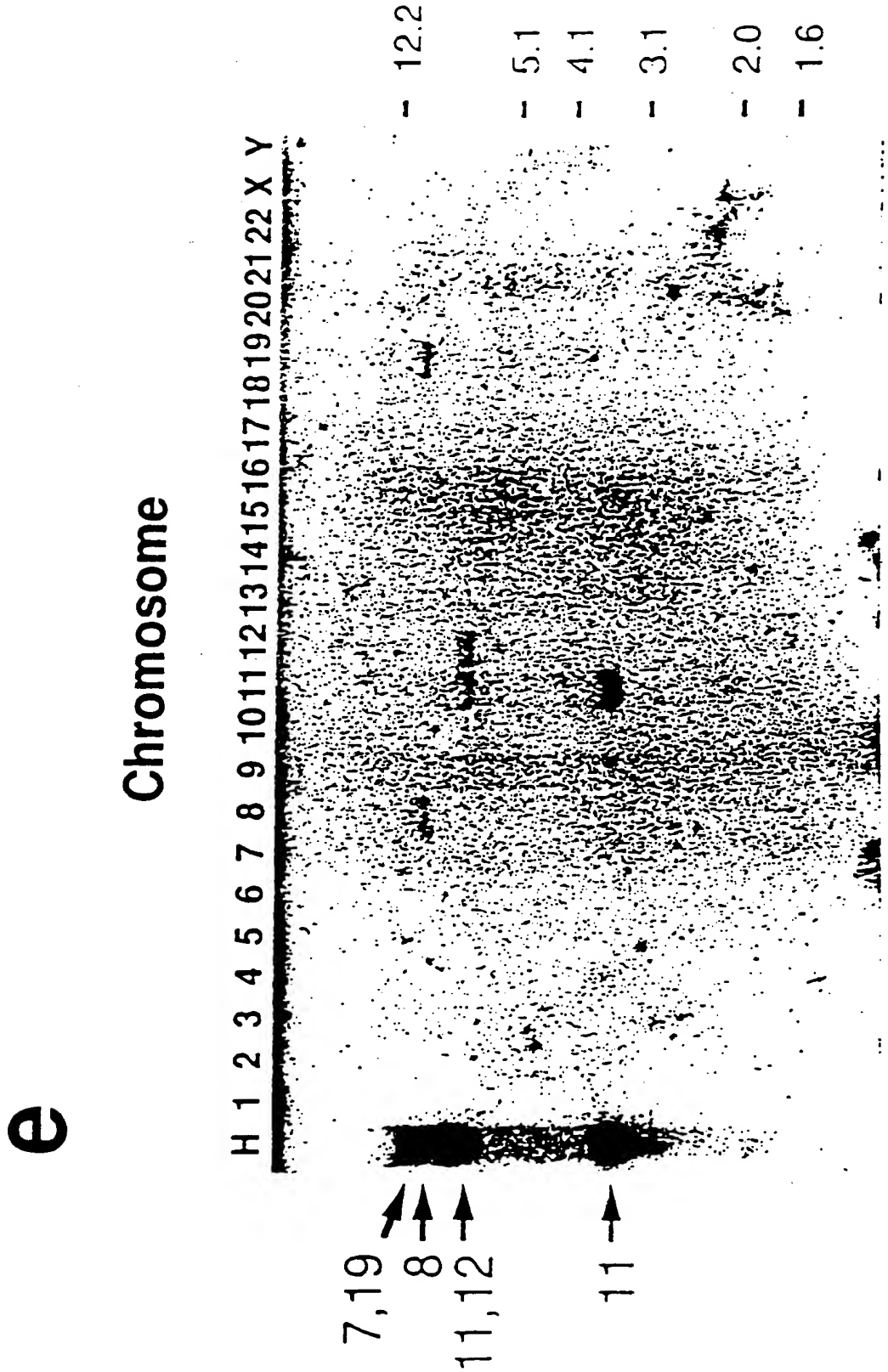
e
Chromosome
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
12.2
5.1
4.1
3.1
2.0
1.6
7,19
8
11,12
11

Fig. 21

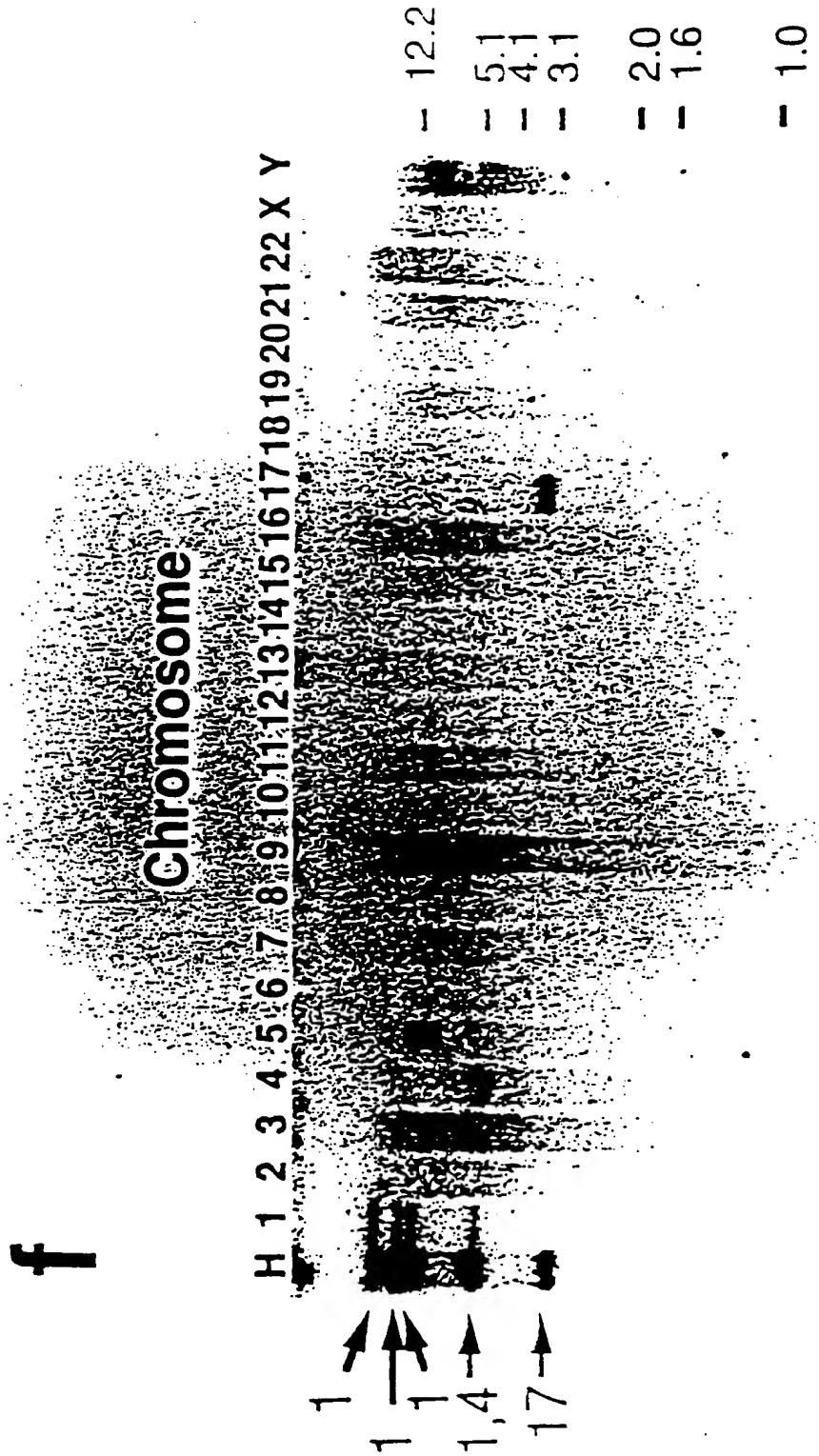

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Fig. 22

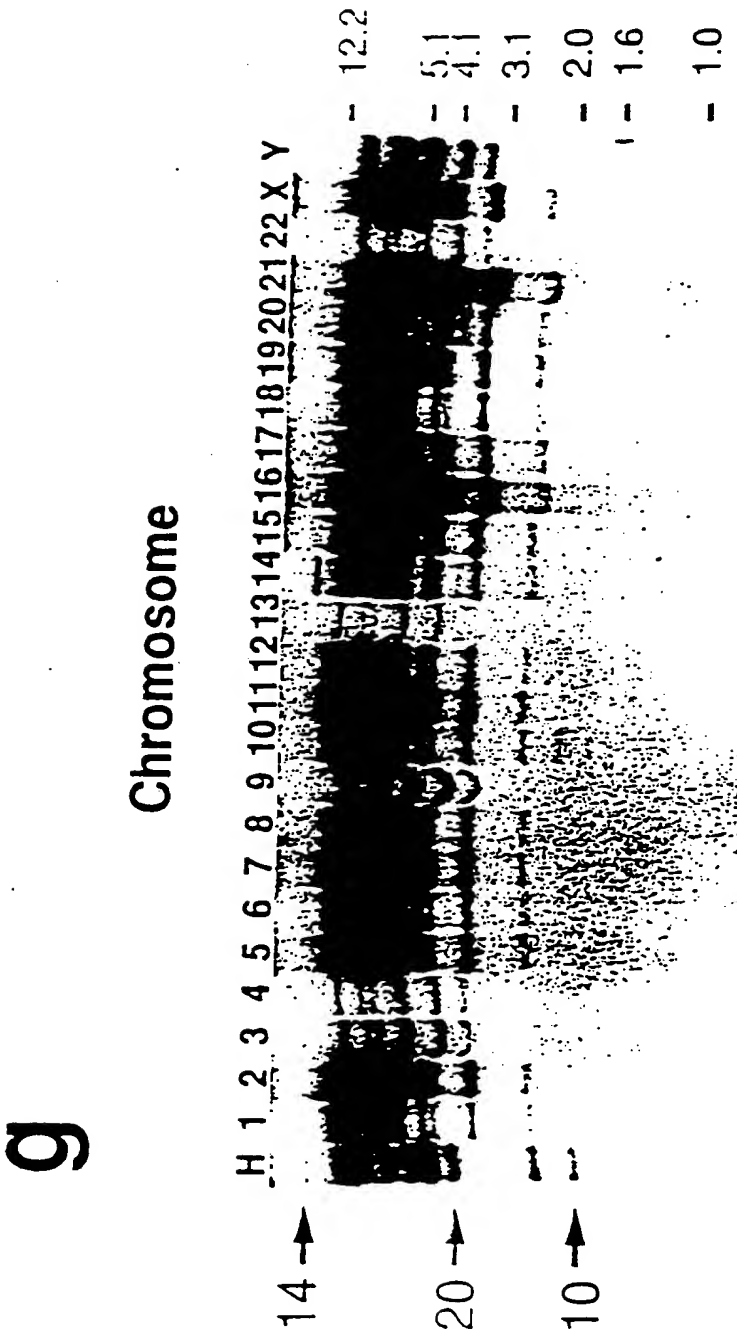
g
Chromosome
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
12.2
5.1
4.1
3.1
2.0
1.6
1.0
14
20
10

Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes							Chromosomes assigned	Background	
Clone		Sequence length	E	E/Ba	E/Bg	Ba/Bg		Mouse	Chinese hamster
Single band group:									
c12e11	GS000075	432	1	1	1	1	9	0	0
c12e06	GS000062	540	1	1	1	1	6,15	0	0
c12g01	GS000290	212	1	1	1	1	2	1	1
c13e05	GS000117	359	1	1	1	1	11-	0	0
c13e07	GS000120	355	1	1	1	1	2	0	0
c13f10	GS000206	267	1	1	1	1	14	0	0
c13h01	GS000279	133	1	1	1	1	13-	0	0
c13h02	GS000322	167	1	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	1	3	0	0
d0h07	GS000134	313	1	1	1	1	11	1	1
d1b10	GS000348	153	1	1	1	1	20	0	0
hm01a12	GS000223	246	1	1	1	1	X?	0	0
hm01e09	GS000423	157	0	1	1	1	1	0	0
hm01e12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19,22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	1	13	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02e01	GS000203	271	1	1	1	1	16	0	0
hm02e01	GS000015	590	1	1	1	1	20	0	0
hm02e02	GS000342	156	0	1	1	1	14	0	0
hm02e05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g02	GS000191	278	1	1	1	1	17	0	0
hm05e05	GS000251	219	1	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	1	0	0
kmc01	junk	169	1	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	1	5	0	0
s110	GS000057	471	1	1	1	1	8	0	0
s11d11	GS000307	#175	0	0	0	1	7	0	0
s11h01	GS000269	204	1	1	1	1	3	0	0
s147	GS000060	461	1	1	1	0	2	0	0
s14e06	junk	639	1	1	1	1	1	0	0
s14g02	GS000152	322	1	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	1	4	1	1
s150	GS000143	330	1	1	1	1	17	0	0
s156	GS000002	306	1	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	1	14	0	0
s179	GS000275	196	1	1	1	1	n.d.	0	0
s246	GS000224	241	1	1	1	1	9	0	0
s247	GS000247	153	1	1	1	1	1	0	0
s270	junk	135	1	1	1	1	19	0	0

Fig. 24

Clone		Sequence length	Numbers of bands detected with human whole chromosomes: E	E/3₂	E/3₅	3₂/3₅	Chromosomes assigned	Background: Mouse	Chinese hamster
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000295	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	261	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	587	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s650	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000218	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-43	GS000096	178	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group :									
c12f12	GS000195	277	1	2	2	2	1,	1	1
c13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,18	3	5
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000181	292	2	2	2	2	1,2	0	0
hm02a08	GS000435	302	2	2	2	2	3,	1	1
hm02e04	GS000221	253	2	2	2	2	3,	0	0
hm02e05	GS000146	332	2	2	2	2	17,19,22	0	0
hm05f07	GS000043	503	1	1	2	1	3,	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6,	0	0
s124	GS000088	404	2	2	2	2	9,	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f08	GS000239	243	1	2	2	2	2,	3	2
s15e02	junk	439	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	284	2	2	2	2	11,	0	0
s254	GS000124	353	2	2	2	2	1,	3	1
s255	GS000235	239	2	2	2	2	11,	0	0
s272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes							Chromosomes assigned	Background	
Clone	Sequence length		E	E/Ba	E/Bg	Ba/Bg		Mouse	Chinese hamster
s311	GS000092	333	1	1	2	2	16.	1	1
s313	junk	182	2	2	1	0	20.	0	0
s317	GS000100	339	0	0	1	2	14,14	1	1
s336	GS000134	337	2	2	2	2	12,14	0	0
s338	GS000139	233	2	2	2	1	22,X	0	0
s339	GS000233	137	2	1	1	2	17.	0	0.
s394	GS000063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GS000236	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s635	junk	250	1	1	1	2	9,13	0	0
s639	GS000257	205	1	2	2	2	2,X	0	0
s656	GS000025	#590	2	2	0	2	6,11	0	0
tw1-33	junk	352	2	2	2	2	1.	0	0
tw1-39	GS000153	#321	2	2	2	2	17.	0	0
tw1-70	GS000061	441	1	1	2	1	11.	0	0
tw1-80	junk	453	2	2	1	2	9,17	2	2
tw1-87	GS000158	316	2	2	2	2	7.	0	0
Three band group									
d0h06	GS000030	417	3	3	3	1	1.	0	0
hm05b07	junk	336	2	3	3	3	5.	0	0.
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s129	GS000107	378	3	3	3	3	n.d.	1	1
s173	GS000357	146	1	2	2	3	2.	0	0
s17a10	GS000294	131	3	3	3	3	2,13,22	1	1
s308	GS000412	638	2	2	2	3	XX	1	1
s401	GS000224	249	2	3	3	3	6,6.	0	0
s654	GS000045	491	3	3	3	3	1,22.	0	0
tw1-82	GS000208	267	3	3	3	3	13.	4	0
Four band group									
c12g07	GS000154	320	4	4	2	3	5, 14.	0	0
c13a08	GS000055	508	3	3	4	4	2,7,7,17	1	2
c13c04	GS000106	#376	4	3	3	3	n.d.	0	2
c13e09	GS000302	195	4	2	4	4	2,17.	7	2
s136	GS000160	315	4	4	4	4	4,X.	2	1
s163	GS000004	#618	4	4	4	2	4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
c12f08	GS000253	217	5	5	5	2	2,7,9,14.	2	0
hc01	junk	374	12	12	15	13	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
he10	junk	173	6	2	3	3	6,8,9,19,21.	3	3
hm01c05	GS000305	176	9	7	5	5	X	9	8
hm01f04	GS000246	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Clone		Sequence length	Numbers of bands detected with human whole chromosomes				Chromosomes assigned	Background	
			E	E/B1	E/B6	B1/B6		Mouse	Chinese hamster
hm02f09	GS000273	442	8	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	GS000096	373	5	6	4	6	2,3,17,	3	3
hm05a04	GS000236	#259	6	6	6	7	n.d.	8	5
kmb01	junk	350	3	5	5	5	13,	14	7
s11f06	GS000315	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3
s14f01	GS000407	262	12	11	10	9	1,6,9,13,	6	5
s173	GS000094	397	5	4	6	8	1,1,1,1,4,17	0	0
s265	GS000323	167	10	12	11	14	18,	9	5
s341	junk	494	9	9	8	6	n.d.	15	3
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X,	3	5
tw1-63	junk	203	8	10	10	12	3,4,	17	11
Bands no detected:									
e13g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP94/01916

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl^6 C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl^6 C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differntiatios, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA:coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
February 6, 1995 (06. 02. 95)	March 7, 1995 (07. 03. 95)
Name and mailing address of the ISA/ Japanese Patent Office	Authorized officer
Facsimile No.	Telephone No.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Batra, S. K. et al. "Molecular cloning and sequence analysis of the human ribosomal protein S16" p. 6830-6833	1-6 (275)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
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X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochim. Bioiphys. Acta., Vol. 1089, 1991, Tamura, T. et al. "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multicatalytic proteinase complexes)" p. 95-102	1-6 (775)
X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
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